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OM nucleic - nucleic search, using sw model

Run on: October 1, 1999, 18:34:56 ; search time 1619 02 Seconds

Run on: October 1, 1999, 18:34:56 ; search time 1619 02 Seconds

Genocre search, using sw model

(*ithout alignments)

Genocre search time 1619 02 Seconds

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Length	638
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		No. Score Match Length DB ID	35
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1 (bases 1 to 35)
Parker, P.J., Goode, N.T., Nurse, P.M. and Waterfield, M.D.
Parker, P.J., Goode, N.T., Nurse, P.M. and Waterfield, M.D.
BUCARYOTIC CELLS TRANSFORMED WITH A MAMMALIAN PHOSPHOLIPID KINASE
OR PROTEIN KINASE AND ASSAYS USING THEM
PATENT: WO 9403609-A 13 17-FEB-1994;
IMP CANCER RES TECH (GB)
Other publication JP 8503124T 960409.
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Mohapatra, S.s. and Sehon, A.H.
DOWNREGULATION OF ALLERGEN-SPECIFIC IMMUNE RESPONSE
PATENT: WO 9425489-A 29 10-NOV-1994;
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100.0%; Score 35; DB 5; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 35; Conservative 0; Mismatches 0; Indels
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Patent: WO 9302195-A 1 04-FEB-1993;
Location/Qualifiers
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Sequence 29 from Patent WO9425489.
A40373
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Sequence 13 from Patent W09403609.
A37244
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A40373.1 GI:2296422
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synthetic construct
artificial sequence.

1 (bases 1 to 35)
Sarmientos, P., De Taxis du Poet, P., Nitti, G. and Scacheri, E.
Anti-thrombin polypeptides
Patent: EP 0501821-A 22 02-SEP-1992;
FARMITALIA CARLO ERBA S.r.L
FARMITALIA CARLO ERBA S.r.L
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Hybrid dT17-adapter primer.
A27645
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NID 91248481
VERSION A27645.1 GI:1248481
KEYWORDS SOURCE synthetic construct.
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1 (bases 1 to 40)
Schuster, E., Sproessler, B., Titze, K., Gottschalk, M., Khanh, N.Q.,
Wolf, S. and Plainer H.
LEUCINE AMINOPEPTIDASES PRODUCED RECOMBINANTLY FROM ASPERGILLUS
                                                                                                                                                                                                                                                                                                                                        unidentified.

unclassified.

NCE 1 (bases 1 to 35)
ORS Knox,D.P., Smith,W.D., Redmond,D. and Murray,J.

S Knox,D.P., Smith,S.K., Smith,W.D., Redmond,D. and Murray,J.

B VACCINES AGAINST HEMINYHIC PARASITES

RALLINGKRODT VETERINARY INC (US)

ALLINGKRODT VETERINARY INC (US)

ALLINGKRODT VETERINARY INC (US)

Other publication CA 212278 951055

Other publication AU 1956495 951017.

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Cocation AU 1956495

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Location/Qualifiers

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1. .35
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Sequence 7 from Patent WO9704108.
A59198
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Sequence 5 from Patent WO9526402.
A46467
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I (bases 1 to 35)

E (bases 1 to 35)

Kamalati,T., Page,M.J. and Spence,P.

RAMALI,T., Page,M.J. and Spence,P.

RAMALET: WO 9502057-A7 19-JAN-1995;

CANCER RES INST (GB)

Other publication AU 7080994 950206.
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Gusterson, B.A., Crompton, M.R., Mitchell, P.J., Barker, K.T.,
Martindale, J.E., Page, M.J. and Spence, P.
CELL GROWTH FACTOR RECEPTORS
Patent: WO 9502187-A 7 19-JAN-1995,
CANCER RES INST (GB)
Other publication AU 7081094 950206.
Location/Qualifiers
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    UNIV MANITOBA (CA)
Other publication AU 6674094 941121.
Location/Qualifiers
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Sequence 7 from Patent WO9502057.
A42335
A42335 A42335 A42335.1 G1:2297812
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Sequence 7 from Patent WO9502187.
A42384
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                                                                                                                                                                                                                                                                     unidentified.
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unclassified.
1 (bases I to 35)
Mele.A., De.S.R., Parente,D. and Colnaghi,M.I.
RECOMBINANT RIBOSOMAL INHIBITOR PROTEIN (RIP) AND USE AS
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Matches 35; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 35)
Adams, M.E. and Zitnan, D.
Ecdysis-triggering hormone compositions
Patent: US 5763400-A 5 09-JUN-1998;
                                                                     Score 35; DB 5;
Pred. No. 0.094;
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PATENT: WO 9749726-A 31-DEC-1997;
MINISTERO UNI RICERCA SCIENT E (IT)
Other publication IT F1960155 19971229.
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
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/organism="unidentified"
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Siegall, C.B.
Cloning and expression of a gene encoding bryodin 1 from Bryonia
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                    Gaps
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Unclassified.
1 (bases 1 to 35)
Sammientos, P., De Taxis du Poet, P., Nitti, G. and Scacheri, E. Sammientos, P., De Taxis du Poet, P., Nitti, G. and Scacheri, E. Anti-thrombin polypeptides
Anti-thrombin polypeptides
Patent: US 5439820-A 35 08-AUG-1995;
Patent: Location/Qualifiers
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Matches 35; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                            Sequence 35 from patent US 5439820.
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ORS Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.

Labavitchs of fungal polygalacturonases and their use to grant inhibitors of fungal polygalacturonases and their use to rentrol fungal disease

Control fungal disease

Control fungal disease

JRNAL Patent: US 556930.A 13 29-OCT-1996;

Source 1.35

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Siegall, C.B., Gawlak, S.L. and Marquardt, H.
Siegall, C.B., Gawlak, S.L. and Marquardt, H.
Bryonia dioica
Bryonia dioica
Patent: US 5597569-A 19 28-JAN-1997;
Location/Qualifiers
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OM nucleic - nucleic search, using sw model

October 1, 1999, 15:36:21; Search time 148.69 Seconds (without alignments) 58.892 Million cell updates/sec Run on:

US-09-026-400-7 35 1 gactcgagtcgacatcgattttttttttttttt 35

Title: Perfect score: Sequence:

IDENTITY_NUC. Scoring table:

311585 seqs, 125096042 residues Searched:

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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3 744 3 1193		11. 1  (33668 standard; cDNA; 35 BP. (33668) (33668) (30568) (30568) (30568) (305-2014-1993 (first entry) PPO adapter primer #1. Polyphenol oxidase; PPO; cata transform, coffee; tea; black transform, coffee; tea; black transform, coffee; tea; black transform; compounds and correase or enhance browning claim 15; Page 23; 44pp; Engl The Sequences given in Q3668 claim 15; Page 23; 44pp; Engl The Sequences given in Q3668 claim 15; Page 23; 44pp; Engl The Sequences given in Q3668 claim 15; Page 23; 44pp; Engl The Sequences given in Q3668 claim 15; Page 23; 44pp; Engl The Sequences given in Q3668 claim 15; Page 23; 44pp; Engl The Sequences given in Q3668 claim 15; Page 23; 44pp; Engl The Sequence given in Q3668-78 ppolyphenol oxidase or enhance browning of fruit caused by plant cells where are stored in the plant cells where and the enzyme and the substr coould be used to construct sytransform plants to decrease increase the level of PPO to increase the plastids of these tissues Sequence 35 BP; 5 A; tches 35; Conservative 0  1 gactcgagtcgacatcgatttttt 1 GACTCGAGTCGACACGATTTTTTT 1 GACTCGAGTCGACACGATTTTTTTT 1 GACTCGAGTCGACACGATTGATTTTTT 1 GACTCGAGTCGACACGATTTTTTTT 1 GACTCGAGTCGACACGATTGATTTTTT 1 GACTCGAGTCGACACGATTTTTTTTT 1 GACTCGAGTCGACACGATTTTTTTTTTTTTTTTTTTTTT
9 9 4 9 		standard; cf  1993 (first  ppter primer  nol oxidase,  nol oxidase,  ppter primer  polymerase  1995.4,  1993.  1992; AU0356  1993; AU0356  1992; AU0356  1992; AU0356  1992; AU0356  1992; AU0356  1993; AU0356  1994; Aucord  103 amin  nol of 660s  10 of
33 33		ESULT 1  136668  103668 standary 109-JUN-1993 ( 109-JUN-1993 ( 1009-JUN-1993 ( 1009-JUN-1994 (
<b>44</b> 45		RESULT 10 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 03666 8 0366
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31-AUG-1994
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Example 1; Page 39; 146pp; English.

Example 1; Page 39; 146pp; English.

Ma SGBAF-1 cell line was established by transfection of bovine adrenal cortex zona faciculata cells with pSV3nco. Total RNA was isolated from the SGBAF-1 and a CDNA library constructed. RACE PCR was performed by synthesising first strand CDNA from random hexamers on SGBAF-1 cell mRNA. PCR was performed using oligo 2224 and adaptord as primers. Products were fractionated using an agarose gel. The DNA was isolated from the gel and subjected to PCR using oligo 2280 and adaptor as primers. A product of 350 bp was further sequenced. Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;
                                                                                                                                                                                                                                                                                                                                           in virus or microbe
Example; Page 32; 137pp; English.
The sequences given in Q52503-11 are primers which were used to amplify cDNA clones of the helminth aminopeptidase genes Hil-1, and -3. The amplified sequences encode Hil0D which is a protein doublet which shows homolgy to a family of integral membrane aminopeptiabases. The differences between the amplified clones can be attributed to different manns of the Hil0D-encoding sequence being present different stages of the life cycle, or in strains different at difference the life cycle, or in strains different at geographical origin. Antigenic fragments of the aminopeptidases encoded by the Hil genes may be used in vaccines to stimulate immune response against helminth parasites in humans or other animals. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequences may be incorporated into a virus or microbe and used in a similar manner. Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;
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Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
antagonist; cell proliferation; inhibition; prophylaxis; therapy;
platelets; neutorphil activity; 3-phosphorylated phosphoinositides;
ss; amplification; pl10.
Synthetic.
                                                                                                                                                                                                                                               WPI; 93-386574/48. New DNA encoding amino-peptidase from Haemonchus contortus and derived peptide(s) - useful in protective vaccines, for new vectors, transformed cells and oligosaccharide, for incorporation
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polymerase chain reaction; amplify; Haemonchus contortus;
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                                                                                                                                                              (AGRI-) AGRIC & FOOD RES COUNCIL.
Graham M, Knox DP, Munn EA, Newton SE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-0CT-1993.
13-APR-1993; G00761.
13-APR-1992; GB-008135.
(LUDW-) LUDWIG INST CANCER RES.
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Best Local Similarity 100.0
Matches 35; Conservative
                                                                                25-NOV-1993.
07-MAY-1993; G00943.
08-MAY-1992; GB-009993.
                                                                                                                                                                                        Graham M, Knox DP,
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WPI; 93-351738/44.
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17-FEB-1994.

17-FEB-1994.

18-05-AUG-1993; GO1651.

PR 05-AUG-1993; GO1651.

PR 05-AUG-1993; GO1651.

PR 05-AUG-1993; GO-16654.

PR 194-06597/08.

PR 294-06597/08.

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                                                                   Gaps
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110 kD catalytic subunit; phosphatidyl inositol 3.kinase; transformation; Schizosaccharomyces pombe; nmt promoter; thiamine; ptdins 3.kinase; assay; detection; cell growth; regulation; cancer; blood vessel plaques; ss.
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W09405795-A.
H7-MRA-1994.
27-AuG-1993; AU0442.
27-AuG-1992; AU-004370.
(CSIR ) COMMOWBALTH SCI & IND RES ORG.
(CSIR ) COMMOWBALTH SCI & IND RES ORG.
FRACI-) PACIFIC SEEDS PIY LTD.
Brady CJ, Lee E, Lester DR, OIT G, Speirs J;
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Length 35;
                                                                      Indels
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Best Local Similarity 100.
Matches 35; Conservative
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                               Q57021 standard; DNA; 35
   Query Match
Best Local Similarity
Matches 35; Conserv
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Seguence 35 BP;
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Example: Page 16; 104pp; English.

The primers given in Q65594-6 were used in the semi-quantitative
The primers given in Q65594-6 were used in the semi-quantitative
PCR detection of HER4.

HER4 is the fourth member of the EGFR-family of tyrosine kinases and
is expressed in some human cancers and in some tissues of neuronal
or muscle origin. HER4 polynocleotides, opt. labelled, are useful
in assays (e.g. of HER4 mRNA to detect certain neoplasms, esp.
breast carcinoma) and as primers in PCR or as probes.

20 T;
                                                                                                                                                                                               Culouscou J, Plowman GD, Shoyab M; WPI; 94-169599/21.
New recombinant nucleic acid expressing HER4 - a new receptor tyrosine kinase expressed in some cancer cells, and related vectors, antibodies, ligands etc, for diagnosis and treatment of
              neuronal tissue; muscle tissue; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Sco...
100.0%; Pred. No. v. o. Mismatches
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24-NOV-1992; US-981165.
(BRIM ) BRISTOL-MXERS SQUIBB CO.
Culouscou J, Plowman GD, Shoyab M;
                                       carcinoma; primer; probe; PCR; ss
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Best Local Similarity 100.
Matches 35; Conservative
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Best Local Similarity 100.
Matches 35; Conservative
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26-APR-1994, CA0228,
26-APR-1993, GB-008581
(UYMA-) UNIV MANITOBA.
                                                                                                         01-JUN-1994.
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              DNA encoding peach polygalacturonase (PG) and production of plants with "melting" or "non-melting" phenotype plants with "melting" or "non-melting" phenotype bisclosure: Page 15: 51pp; English.

During early ripening of peaches, tissue firmness decreases is alowly and progressively. Towards the end of ripening, loss of tissue firmness; is rapid. This second stage of softening is called the "melting" stage. Fruit of peach varieties used for canning do not have a "melting" phase of softening. Ripe fruit remain relatively firm and maintain their shape throughout processing. Fruit of "melting" varieties show an increase in activity of endopolygalacturonase (Endops) during ripening. Polygalacturonase (Endops) during ripening. Polygalacturonase (Endops) during ripening through its action on intercellular and cell wall pectins. This primer was used to synthesise a first strand cDNA molecule for further amplification or process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1994 (first entry)
T cell protein CD4 adaptor-dT17 primer.
Cat: feline immunodeficiency virus; CD4 positive T lymphocyte;
cellular receptor; T cell protein; polymerase chain reaction; PCR; ss.
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Human epidermal growth factor receptor; HER; EGF; tyrosine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodefictency virus and for therapy
Disclosure; Page 5; 25pp; French.
The primers Q63811 and Q63872 were used to obtain cDNA coding for
feline CD4 protein by polymerase chain reaction. For rapid
amplification of the ends of the CDNA, a hybrid adaptor-oligo(dT)
primer was also used. Cat lymph node CDNA was amplified and the
full.length CD4 coding sequence Q63870 was obtained from several
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G;
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25-SEP-1992; 011496.
25-SEP-1992; FR-011496.
(UYPA-) UNIV CURIE PARIS VI P & M.
De Parseval A, Klatzmann D, Salmon P,
WPI; 94-128285/16.
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C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q65594 standard; DNA; 35 BP
                                                                                                                                                                                                                                                                                                                                                                                               5 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          063873;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Q63873
NAME OF THE PART O
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Gaps

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0; Indels

Score 35; DB 1; Length 35; Pred. No. 0.011;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody production against allergenic antigen (Ag) is specifically suppressed by treatment with the junctional segment of the alpha and/or beta chain of the Ag receptor of suppressor T (TS) cells (TCR) induced by tolerogenic Ag-PBG conjugates. CDNAs encoding the alpha and beta chains of TCRs of cloned Ts cells specific for ovalbumin and human monoclonal (myeloma) IgG were produced by PCR using the primers given in Q78798-805 and the adaptors given in Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                 Mohapatra SS, Sehon AH; WPI; 94-358193/44. Synthetic peptide(s) for effecting immuno:therapy - have an amino acid sequence comprising a portion of the CDR3 region of a T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 35; 0.011;
                                                            Allergen; immunotherapy; T-cell receptor; TCR; CDR3; complementarity determining region-3; immunosuppressive antibody engineering; suppressor T-lymphocyte; Ts; PCR; polymerase chain reaction; amplification; adaptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 43; 78pp; English.
12-JUN-1995 (first entry)
TCR alpha-chain dT17 adaptor.
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Gaps

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New ribosome inactivating protein bryodin-2 and related conjugates - for killing target cells, e.g. in treatment of cancer, also related nucleic acid, vectors and transformed cells Disclosure; Page 43: 81pp; English.

The sequence is that of a PCR primer used to isolate a ribosome inactivating protein termed bryodin-2, from Bryonia dioica. Conjugates of the protein with a ligand may be used to kill target cells (i.e. those to which the ligand component binds specifically) or to inhibit proliferation of tumour cells. Typical applications include the treatment of cancer, viral infections, malaria, trypanosomiasis, inflammatory or autoimmune diseases, including in vitro purging of e.g.
                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1995 (first entry)
CKR primer for cloning bryodin-2.
Ribosome inactivating protein; cell death; proliferation; tumour; cancer; virus; malaria; trypanosomiasis; inflammation; autoimmune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-APR-1996 (first entry)
Oligonucleotide probe for human prostacyclin-synthase.
Oligonucleotide probe for human prostacyclin-synthase.
DNA primer; prostacyclin-synthase; PCR; polymerase chain reaction;
DNA primer; prostacyclin-synthase; PCR; polymerase chain reaction;
DNA primer; prostacyclin-synthase; PCR; polymerase chain reaction;
Synthetic:
W09530013-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 95-393084/50.
Human prostacyclin synthase and DNA encoding it - useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  incorrect cross reference numbers. 5 C; 5 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 1; Length 35; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
             100.0%; Score 35; DB 1;
100.0%; Pred. No. 0.011;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 gactcgagtcgacatcgatttttttttttttt 35
                                                                                                             1 gactcgagtcgacatcgattttttttttttttt 35
                                                                                                                                                                1 GACTCGAGTCGACATCGATTTTTTTTTTTTTT 35
                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO.
Gawlak SL, Marquardt H, Siegall CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               purging; bone marrow; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105321 standard; DNA; 35 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also 089874-86.
Updated 31-JAN-1997 due to
Sequence 35 BP; 5 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 35; Conservative
                                                                  Conservative
                                                                                                                                                                                                                                                                                              Q89878 standard; DNA; 35
Q89878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-1995.
25-OCT-1994; U12382.
25-OCT-1993; US-141891.
20-OCT-1994; US-324301.
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27-APR-1995; JO0838.
28-APR-1994; JP-114316.
(TANA/) TANABE T.
                                                                                                                                                                                                                                                                                                                                                 (Revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gawlak SL, Marqua
WPI; 95-178870/23.
                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone marrow
                                                                                                                                                                                                                                                                                                                                                    31-JAN-1997
                                             Best Local Sim
Matches 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I Barker KT, Crompton MK, Gusterson BA, Martinuare DE;

Mitchell PJ, Page MJ, Spence P;

Mutchell PJ, Page MJ, Spence P;

Mutchell PJ, Page MJ, Spence P;

WPI; 95-066991/09.

WPI; 95-066991/09.

Method for screening substances, using protein tyrosine kinase -
for potential utility as therapeutic agents for cancer

Disclosure; Page 34; 51pp; English.

C DNA derived from tumor metastatic tissue was amplified using

C DNA derived from tumor metastatic tissue was amplified using

C DNA derived from tumor metastatic tissue was amplified using

C Sascoiated with protein-tyrosine-kinases (PTK). Novel PTK22 was

C dentified in an isolated subclone. The 3' sequence of PTK22 was

C dentified in an isolated subclone. The 3' sequence of PTK22 was

C patrined by reverse transcription (using the primer of 084786) and

C carcinoma cell line MDA MG 468. The partial DNA sequence of PTK22

C sarcinoma cell line MDA MG 468. The partial DNA sequence of PTK22

Sequence 35 BP; 5 A; 5 C; 5 G T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WELL MANAGEMENT OF TOTAGE WAY TO TOTAGE WAY WELL STATE WHIT 95-195588/26.

New Japanese cedar pollen allergen polypeptide - and DNA coding for New Japanese cedar pollen allergen polypeptide - and allergy Disclosure: Page 11: 41pp; English.

Disclosure: Page 11: 41pp; English.

Disclosure: page 11: 41pp; English.

English aportion of cDNA clone aportion of cDNA clone amplification of cDNA derived from Japanese cedar pollen, to obtain clone SC50 bearing a partial sequence (nt 1198 of the sequence siven in 090155) of the pollen allergen gene.

Sequence 35 BP; 5 A; 5 C; 5 G;
                                                                                                                                                                           17-AUG-1995 (first entry)
PTK22 reverse-transcription primer.
Protein-tyrosine-kinase; PTK; discoidin domain receptor; cancer;
breast tumor; mamma carcinoma; diagnosis; prognosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pollen allergen gene primer 8.
Japanese cedar; pollen; allergen; allergy; therapy; diagnostic; desensitizer; Cryptomeria japonica; polymerase chain reaction; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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19-JUL-1994; G01480.

09-JUL-1993; GB-014271.

(CAMC.) CANCER RES INST.

(WELL) WELLCOME FOUND LID.

BATEN RT. Crompton MR. Gusterson BA, Martindale JE;

BATEN RT. Crompton MR. Gusterson BA, martindale JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GACTCGAGTCGACATCGATTTTTTTTTTTTTTTT 35
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1 GACTCGAGTCGACATCGATTTTTTTTTTTTTT
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Kurimoto M, Namba M, Torigoe K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090167 standard; DNA; 35 BP
                                                                                                                             084786 standard; DNA; 35 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-NOV-1994; 308117.
05-NOV-1993; JP-299151.
20-DEC-1993; JP-344596.
27-DEC-1993; JP-346814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 35; Conserv
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Query Match

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Gaps

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respiratory disease;

Takagi K;

Query Match

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Muria variable variab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-1996 (first entry)
Trypsin-like enzyme N-terminal DNA fragment from p19-33.
Trypsin-like enzyme N-terminal by fragment; respiratory disease; Trypsin, fibrinogen; thrombin; expectorant; respiratory disease; asthma; VIP; vasoactive intestinal peptide; influenza virus; protease; primer; PCR; amplification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases, e.g. bronchial asthma
Example 9; Page 44-45; 65pp; English.
Example 9 describes the cloning of CDNA region encoding
Example 9 describes the cloning of English.

Four oligonucleotides are used for PCR: TRY-1 (T10694), TRY-8
(T10695), TRY-10 (T10696) and TRY-11 (T10697).

TRY-1 corresponds to from Al to A23 of the sequence given in T10693, which is part of a cDNA encoding the trypsin-like enzyme. TRY-8 corresponds to from G16 to T40 of T10693.
                                                                                         26-MAY-1996 (first entry)
Trypsin-1ike enzyme oligonucleotide TRX-10.
Trypsin; fibrinogen; thrombin; expectorant; respiratory dise asthma; VIP; vasoactive intestinal peptide; influenza virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 35; DB 1; Length 35; 100.0%; Pred. No. 0.011; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suga T, Sugimoto Y, Takagi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gactcgagtcgacatcgattttttttttttttt 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suga T, Sugimoto Y,
                                                                                                                                                                                                                                                        protease; primer; PCR; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T10698 standard; cDNA to mRNA; 901 BP
                 r10696 standard; DNA; 35 BP.
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29-JUL-1994; JP-178607.
(TELI ) TELJIN LTD.
Masuda K, Ogawa H, Suga
Yamaoka K, Yasuoka S;
WPI; 96-117356/13.
                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-1995; 027248.
29-JUL-1994; JP-178607.
(TELT) TEIJIN LTD.
Masuda K, Ogawa H, Suga
Yamaoka K, Yasuoka S;
WPI; 96-117356/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
AU9527248-A.
                                                                                                                                                                                                                                                                                               Synthetic.
AU9527248-A.
08-FEB-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-1996.
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investigation and treatment of diseases characterised by reduced prostaglandin 12 production.

Subscioure: Page 34: 71pp: Japanese.

Discloure: Page 34: 71pp: Japanese.

Discloure: Page 34: 71pp: Japanese.

DNA primers (705317-20; 705325: 705326-27) are used to screen human comparing to the isolation of a prostacyclin-synthase (PGIS) coding sequence (see 705316). DNA probes (705321 and 705323) are used in the construction of plasmid pHPGIS1, encoding the complete PGIS sequence. This plasmid was used to transfect human 293 cells for petted expression. DNA encoding human PGIS, vectors containing it, and PGIS itself, may be administered to patients to increase prostaglandin 12 PGIS1 production to treat diseases characterized by reduced PGIS levels or by an imbalance between PGI2 and thromboxane A2 levels, such as circulatory diseases (thrombosis, angina pectoria arteriosclerosis, myocardial infarction). The Sequence 35 BP; 5 A; 5 C; 5 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1996 (first entry)
Cysteine proteinase active site antisense polyT primer.
Cysteine proteinase active site antisense polyT primer.
Cysteine proteinase DM.2: DM.3: DM.4; human; DM.4a; DM.5; antigen; vaccine; helminth; parasite; DM.1; ruminant; gastro-intestinal tract; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knox DP, Murray J, Redmond D, Smith SK, Smith WD;
WPI: 95-35132245.

Protective helminth parasite antigen - used in vaccine directed against parasitic nematodes of mammalian gastro-intestinal tract e.g. Haemonchus contortus

Example 16; Fig 15; 79pp; English.

The sequences given in 094240-45 are primers which are based on previously published sequences derived from the canonical Haemonchus contortus cysteine proteinase molecule. These primers were used in the cloning of cDNA fragments from the cysteine protienase gene, such as DM.1, DM.2, DM.3, DM.4, DM.4a and DM.5 (see also Q94246-51). The amplified fragments may be expressed in a recombinant cell for the production of antigens. These antigens may be used in the production of a vaccine against helminth parasites in a human or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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24-MAR-1995; G00665.
25-MAR-1994; GB-005990.
25-MAR-1994; GB-005925.
KMLW ) MALLINCKRODT VETERINARY INC.
KNOX DP, MULTAY J, REGMODG D, SMI
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Query Match Best Local S

Matches

14

RESULT T10696

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Sequence

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Gaps

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TRY-10 is capable of annealing to the 3'-terminus of poly(A)+ RNA. TRY-11 is identical to the 5'-terminus side 19 residues of TRY-10. After amplification, plasmid p19-33 was obtained. p19-33 encodes part of the N-terminus amino acid sequence 20 residues of the trypsin-like enzyme isolated from the cough phiegm (see T10698). Sequence 901 BP; 270 A; 185 C; 205 G; 241 T;
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Search completed: October 1, 1999, 15:36:23 Job time: 6121 sec

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October 1, 1999, 15:03:42; search time 1096.08 Seconds (without alignments) 62.987 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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Perfect score:
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A1295887 LP09649.5
A139226 FEST46034
A139226 FEST4603.X
A131226 FEST4603.X
A137729 UT.R-YO-a
L38011 BNRPC2511.X
A1541359 INIGHIS5
AA7241359 INIGHIS5
AA724189 INIGHIS5
AA724189 INIGHIS5
AA724189 INIGHIS5
AA73239 INIGHIS35
AA732415 GW3400.X
AI254415 GV4610.X
AI254415 GV4610.X
AI254415 GV4610.X
AI26430 GW48300.X
AI26430 GW8300.X
AI36531 GW7660.X
AI36531 GW7660.X
AI36531 GW7060.X
AI366353 GW80300.X
AI366353 GW80300.X
                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA340759 337 bp mRNA EST 21-APR-1997 EST46034 Fetal kidney II Homo sapiens cDNA 5' end similar to similar to protein phosphatase 2A, beta, 55 kDa, mRNA sequence. AA340759 g1992998 AA340759.1 GI:1992998
                                                                                                                                    Description
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AI56751
AI58011
AI725205
AI7205
AI725205
AI72505
AI72
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A1254455
A1254797
A1254907
A1255106
A1255106
A1271282
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AI284843
em_est22:*
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em_est26:*
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Elthoria; Primates; Catarrhini; Hominidae; Homo.

Sala, C., Cataron, G., Blake, J.R., Freischmann, R.D., Fuldner, R.A., Mantwal, C.,

Mhite, O., Sutton, G., Blake, J.R., Brandon, R.C., Mantwal, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Ghehm, C.L., Hanna, M.C., Hedblancs, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Moreno-Palanques, R.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, T.B., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.A.,

Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

NE Nature 377 (6547 Suppl.), 3-174 (1995)
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LP09649.5prime LP Drosophila melanogaster larval-early pupal pOT2
Drosophila melanogaster cDNA clone LP09649 5prime, mRNA sequence.
AI295887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on Sep 12, 1996 this sequence version replaced gi:1406936.
Other_ESTs: EST46035 THC125647
Contact: Kerlavage, AR
Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research y12 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423
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Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="ATCC (inhost):142407"
/db_xref="taxon:9606"
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ta78e03.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050204 3',
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Email: Robert Strausbergenih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LP Drosophila melanogaster larval-early pupal
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 111)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.cip.geov.ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //sex="male and female"
//dev_stage="larvae-pupae"
//lab_host="Day=apha"
//note="Organ: whole body; Vector: pOT2; Site_1: EcoR1;
Site_2: Mo1; Sized fractionated cDNAs were directly
ligated into pOT2. Plasmid cDNA library.
                                                                                                                                                                                                                                                              G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 B4747
Fax: 510 LPD://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 96 row: E column: 1
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Unpublished (1997)
On Feb 10, 1998 this sequence version replaced gi:2340789.
                                                                                                                                                                Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:2044369.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 678)
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                                                                                  Pendleton, J., Su, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LP09649"
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0; Mismatches
                                                                                Harvey,D., Hong,L., Evans-Holm,M., Per
Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
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Best Local Similarity 87.5
Matches 28; Conservative
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224 c
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AI568751
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Best Local Simi
Matches 29;
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KEYWORDS
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@hih.gov
Email: Robert_Strausberg@hih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1348883 380 bp mRNA EST 16-FEB-1999 tb05c11.x2 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052692 3/ similar to contains Alu repetitive element; contains L1.t2 L1 repetitive element; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
On Aug 21, 1998 this sequence version replaced.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 380)
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                round through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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/clone="INAGE:2052692"
/clone="INAGE:2052692"
/tissue_tipe="invasive adenocarcinoma"
/dev_stage="adult"
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                                                                                                                 1. 111 // Organism="Homo sapiens" // Organism="Homo sapiens" // Object="taxon:9606" // Clone="IMAGE:2050204" // Clone_lib="NCI_CGAP_HSC2" // Lissue_Lype="stem cell 34+/38+" // dev_stage="adult" // Iab_host="DH10B"
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                                                                         Seq primer: -400P from Gibco.
Location/Qualifiers
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AI348883.1 GI:4086089
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AI34883
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="llpil"
/clone="libe"Nct_CGAP_CLLI"
/clone="Inba"Nct_CGAP_CLLI"
/clone="type="B-cell, chronic lymphotic leukemia"
/clone="type="type="type="cell"
/clone="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="type="
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th.5009.xl NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2118353 3',
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/lab_host="DH10B"
/note="Organ: lung; Vector: pAMP1; mRNA made from lung adenocarcinoma tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average linsert size 500 bp. Primary library, non-amplified.
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., M.D., M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cen
Clone distribution: NCI-CGAP clone distribution information ca
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
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Unpublished (1997)
On Feb 18, 1999 this sequence version replaced g1:4297567
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Gaps

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Brassica rapa
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae, eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L38011 305 bp mRNA EST 07-NOV-1996
BNAF0228E Mustard flower buds Brassica rapa cDNA clone F0228, mRNA
bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C18175 435 bp mRNA EST 02-OCT-1996 C18175 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-558E05 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed sequence tags of Chinese cabbage flower bud cDNA Plant Physiol. 111 (2), 577-588 (1996)
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                                                                                                                                                                                                                                                                 Query Match 72.6%; Score 25.4; DB 51; Length 466; Best Local Similarity 82.9%; Pred. No. 2.6e+02; Matches 29; Conservative 0; Mismatches 6; Indels 0;
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1 Similarity 92.9%; Pred. No. 4.3e+02;
26; Conservative 0; Mismatches 2;
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/note="Devel_stage = flower bud
50 c 52 g 98 t
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/organism="Brassica_rapa"
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TAG_TISSUE=Eye
TAG_SEQ=CATTG"
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// (Jone="UTR-Y0" acq-h-01-0-UI"
// (Jone="UTR-Y0" acq-h-01-0-UI"
// (Joub_host="DH10B (Life Technologies)"
// (hote="Vector: pT773D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco Ri; The UTR-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UTR-A0, UTR-A1, UTR-E0,
UTR-E1, UTR-C0, and UTR-C1). The tag is a string of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UTR-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTS had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
Enail: msoarces@blue.weeg.uiowa.edu
Coligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soarces Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seg primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 466)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                             AI717729 466 bp mRNA EST 10-JUN-1999 UI-R-YO-acq-h-01-0-UI.s1 UI-R-YO Rattus norvegicus CDNA clone UI-R-YO-acq-h-01-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On May 18, 1998 this sequence version replaced gi:3138263.
                                                                                                         ó
                                                            Length 909;
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
                                                            48;
                                                                                                       9;
                                                            Score 25.4; DB 4
Pred. No. 2e+02;
0; Mismatches

    466
    /organism="Rattus norvegicus"

                                                                                                                                                       discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Sprague-Dawley
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                             95034985
AI717729.1 GI:5034985
                                                          Query Match 72.6%;
Best Local Similarity 82.9%;
Matches 29; Conservative
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Rattus norvegicus
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AI717729
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Gaps

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/tissum_type="metastatic prostate bone lesion"
/lab_host="DHIOB"
/note="Vector: pAMPIO; mRNA made from metastatic prostate
lesion of the bone, cDNA made by oligo-dr priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gössypium hirsutum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 466)
Blewitt,M., Matz.B.C., Davy,D.F. and Burr,B.
ESTS from developing cotton fiber
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI726205 466 bp mRNA EST 11-JUN-1999
BNLGH15252 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (Y09741) beta-tubulin 1 [Hordeum vulgare], mRNA sequence.
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/oultivar="Acala Maxxa"
/db_xxef="taxon:3853"
/db_xxef="taxon:3853"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="Xi1-Blue"
/note="Vector: pBluescript II KS+"
3 a 118 c 71 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.3%; Score 24.6; DB 35; Best Local Similarity 87.1%; Pred. No. 4.8e+02; Matches 27; Conservative 0; Mismatches 4;
                                                    Insert Length: 389 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 273.
      ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                     1. .314
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:982855"
/clone_lib="NCI_CGAP_Pr12"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                            100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biology Department
Brookhaven National Laboratory
Upton, NY 11973 USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
Seq primer: 73 Primer.
Location/Qualiflers
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                                                                                                                                                              I (bases 1 to 435)
Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,
Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y.,
Shimomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T.,
Otsuka cDNA project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1392743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert_Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA541358 314 bp mRNA EST 19-AUG-1997
ni77d04.sl NCI_CGAP_Prl2 Homo sapiens CDNA clone IMAGE:982855, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                 Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 314)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-558E05"
/clone_lib="Human placenta cDNA (TFujiwara)"
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Pred. No. 3.8e+02;
0; Mismatches 2;
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88 c 111 g 10
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AA541358
92287792
AA541358.1 GI:2287792
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C18175
91579777
C18175.1 GI:1579777
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                                                                                                          Homo sapiens
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Best Local Similarity
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                                                                                   human.
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AA541358/C
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Homo sapiens
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                                                                                                                                                                                                                                                             AI729852 623 bp mRNA EST 11-JUN-1999
BNLGH15355 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
to (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                         Gaps
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               Length 466;
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                                         Indels
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/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="Xi1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript II KS+" 178 c 90 g 195 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24.6; DB 51;
Pred. No. 3.7e+02;
0; Mismatches 4;
           Query Match 70.3%; Score 24.6; DB 51; Best Local Similarity 87.1%; Pred. No. 4.2e+02; Matches 27; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gossypium hirsutum"
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Brookhaven National Laboratory
Upton, Nr 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
Email: burrebnlux1.bnl.gov
Seq primer: T3 Primer.
Location/Qualifiers
e 1. 623
                                                                                 5 cgagtcgacatcgattttttttttttttt 35
                                                                                                                                                                                              sativa], mRNA sequence.
AI729852
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AA541329
92287763
AA541329.1 GI:2287763
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Best Local Similarity 87.1%;
Matches 27; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ben Burr
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                                                                                                                                                                                                                                                                                  ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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SOURCE
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                                                                                                                                    RESULT 1
AI729852
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/lab_host="PH10B"
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lesion of the bone, CDNA made by Oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Library made by D. Krizman,
                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,
Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Bukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 511)

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research,

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

On Mar 10, 1998 this sequence version replaced gi:2948982.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 405) NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap. NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 421 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 126.
Location/Qualifiers
1. .405
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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AA145612.1 GI:1715011
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Best Local Similarity 82.4:
Matches 28; Conservative
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AA145612
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CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Rashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
www-bio.llnl.gov/bbrp/image/image.html
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0
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This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -400p from Gibco
High quality sequence stop: 432.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primeres; Catarrhini; Hominidae; Homo.

(Dases 1 to 517)

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Enstitute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Dec 20, 1995 this sequence version replaced gi:1134555.

Other_ESTs: nc78e12.x5
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69.7%; Score 24.4; DB 51; Length 511;
Best Local Similarity 82.4%; Pred. No. 4.5e+02;
Matches 28; Conservative 0; Mismatches 6; Indels 0;
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95055301
AI734188.1 GI:5055301
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ORIGIN
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TITLE
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AI734188
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINK at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 570)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone
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IMAGE:606307 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2
(HUMAN);, mRNA sequence.
Aa145612
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Pred. No. 4.5e+02;
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High quality sequence stop: 417.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1292118.
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69.1%; Score 24.2; DB 29; Length 570;
Best Local Similarity 89.7%; Pred. No. 4.9e+02;
Matches 26; Conservative 0; Mismatches 3; Indels 0.
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Search completed: October 1, 1999, 15:03:44 Job time: 4388 sec

314 AGCTGACATCGAGTTTTTTTTTTTTTTTT 342